1. (Amended) A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

(a) providing a population of nucleic acid fragments at least some of which have sequences that are repeated more than once in a genome;

(b) incubating single stranded forms of the population of nucleic acid fragments under annealing conditions, whereby single stranded forms of nucleic acid fragments having repeat sequences preferentially hybridize to each other relative to nucleic acid fragments lacking repeat sequences;

(c) separating single stranded forms of the population of nucleic acid fragments from annealed double stranded forms, the single stranded forms being enriched for nucleic acid fragments lacking repeat sequence and the annealed double stranded forms being enriched for nucleic acid fragments containing repeat sequences;

A1

(d) hybridizing the separated single stranded forms of the population of nucleic acid fragments, wherein said separated single stranded forms are enriched for nucleic acid fragments lacking repeat sequence, to a nucleic acid probe array, which array comprises a set of probes complementary to a known reference sequence, the reference sequence being the same or a variant of the sequence of a nucleic acid from which the population of nucleic acid fragments was obtained; and

(e) determining hybridization of the probes to the single stranded forms of the population of nucleic acid fragments, wherein said single stranded forms are enriched for nucleic acid fragments lacking repeat sequence, thereby analyzing said subset of nucleic acids within said nucleic acid population.

13. (Amended) The method of claim 1, wherein the determining indicates the presence of at least one variation in a fragment hybridized to the array relative to the reference sequence.

A2

14. (Amended) The method of claim 1, wherein the population of nucleic acids are from a chromosome from a first individual, and the reference sequence is that of a corresponding chromosome from a second individual.

15. (Amended) A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

(a) providing driver and tester populations of nucleic acids;

(b) hybridizing the driver and tester populations with each other;

(c) separating nucleic acids from the tester population that hybridize to the driver population from tester nucleic acids that do not hybridize;

(d) hybridizing either the tester nucleic acids that do hybridize to the driver population, or the tester nucleic acids that do not hybridize to the driver population to a nucleic acid probe array, wherein said array comprises a set of probes complementary to a known reference sequence, the reference sequence being the same or a variant of the sequence of a nucleic acid from which the nucleic acid population was obtained; and

(e) determining hybridization of the probes to the tester nucleic acids thereby analyzing the tester nucleic acids.

A2

16. (Amended) The method of claim 15, wherein nucleic acids in the driver population each bear a tag by which nucleic acids in the driver population can be immobilized to a binding moiety with affinity for the tag.

18. (Amended) The method of claim 16, wherein the separating step is performed by immobilizing the driver population of nucleic acids and tester population of nucleic acids hybridized to the driver population via the tags of the driver population.

A3

35. (Amended) The method of claim 15, wherein the population of driver nucleic acids are mRNA or nucleic acids derived therefrom from a first source, and the population of tester nucleic acids are mRNA or nucleic acids derived therefrom from a second source, the tester nucleic acids that do not hybridize with the driver nucleic acids are hybridized to the array, these tester nucleic acids being enriched for sequence present in the second source and absent in the first source.

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